

In the specification:

Please insert the following as a sequence listing in the specification. A separate copy is enclosed.

SEQUENCE LISTING

<110> Liao and Zeldin

<120> ANTI-INFLAMMATORY ACTIONS OF CYTOCHROME P450 EPOXYGENASE-DERIVED EICOSANOIDS

<130> 4239-62631/WDN/SLR

<140> US 09/634,369

<141> 2000-08-09

<150> US 60/148,434

<151> 1999-08-11

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 1020

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1020)

<223>

<400> 1

gct gac ttt ctc aaa aga cgg cgc cca aag aac tac ccg ccg ggg ccc	48
Ala Asp Phe Leu Lys Arg Arg Arg Pro Lys Asn Tyr Pro Pro Gly Pro	
1 5 10 15	

tgg cgc ttg ccc ttc ctt ggc aac ttc ttc ctt gtg gac ttc gag cag	96
Trp Arg Leu Pro Phe Leu Gly Asn Phe Phe Leu Val Asp Phe Glu Gln	
20 25 30	

tcg cac ctg gag gtt cag ctg ttt gtg aag aaa tat ggg aac ctt ttt	144
Ser His Leu Glu Val Gln Leu Phe Val Lys Lys Tyr Gly Asn Leu Phe	
35 40 45	

agc ttg gag ctt ggt gac ata tct gca gtt ctt att act ggc ttg ccc	192
Ser Leu Glu Leu Gly Asp Ile Ser Ala Val Leu Ile Thr Gly Leu Pro	
50 55 60	

tta atc aaa gaa gcc ctt atc cac atg gac caa aac ttt ggg aac cgc	240
Leu Ile Lys Glu Ala Leu Ile His Met Asp Gln Asn Phe Gly Asn Arg	
65 70 75 80	

RECEIVED
TECH CENTER
03 APR 28 AM 9:55
1600/2900

ccc gtg acc cct atg cga gaa cat atc ttt aag aaa aat gga ttg att	288
Pro Val Thr Pro Met Arg Glu His Ile Phe Lys Lys Asn Gly Leu Ile	
85 90 95	
atg tca agt ggc cag gca tgg aag gag caa aga agg ttc act ctg aca	336
Met Ser Ser Gly Gln Ala Trp Lys Glu Gln Arg Arg Phe Thr Leu Thr	
100 105 110	
gca cta agg aac ttt ggt tta gga aag aag ggc tta gag gaa cgc att	384
Ala Leu Arg Asn Phe Gly Leu Gly Lys Lys Gly Leu Glu Glu Arg Ile	
115 120 125	
cag gag gag gcc caa cac ctc act gaa gca ata aaa gag gag aac gga	432
Gln Glu Glu Ala Gln His Leu Thr Glu Ala Ile Lys Glu Glu Asn Gly	
130 135 140	
cag cct ttt gac cct cat ttc aag atc aac aat gca gtt tcc aat atc	480
Gln Pro Phe Asp Pro His Phe Lys Ile Asn Asn Ala Val Ser Asn Ile	
145 150 155 160	
att tgc tcc atc acc ttc gga gaa cgc ttt gag tac cag gat agt tgg	528
Ile Cys Ser Ile Thr Phe Gly Glu Arg Phe Glu Tyr Gln Asp Ser Trp	
165 170 175	
ttt cag cag ctg ctg aag tta cta gat gaa gtc aca tac ttg gag gct	576
Phe Gln Gln Leu Leu Lys Leu Asp Glu Val Thr Tyr Leu Glu Ala	
180 185 190	
tca aag aca tgc cag ctc tac aat gtc ttt cca tgg ata atg aaa ttc	624
Ser Lys Thr Cys Gln Leu Tyr Asn Val Phe Pro Trp Ile Met Lys Phe	
195 200 205	
ctg cct gga ccc cac caa act ctc ttc agc aac tgg aaa aaa ctg aaa	672
Leu Pro Gly Pro His Gln Thr Leu Phe Ser Asn Trp Lys Lys Leu Lys	
210 215 220	
ttg ttt gtt tct cat atg att gac aaa cac aga aag gat tgg aat cct	720
Leu Phe Val Ser His Met Ile Asp Lys His Arg Lys Asp Trp Asn Pro	
225 230 235 240	
gca gaa aca aga gac ttt att gat gct tac ctt aaa gaa atg tca aag	768
Ala Glu Thr Arg Asp Phe Ile Asp Ala Tyr Leu Lys Glu Met Ser Lys	
245 250 255	
cac aca ggc aat cct act tca agt ttc cat gaa gaa aac ctc atc tgc	816
His Thr Gly Asn Pro Thr Ser Ser Phe His Glu Glu Asn Leu Ile Cys	
260 265 270	
agc acc ctg gac ctc ttc ttt gcc gga acc gag aca act tcc aca act	864
Ser Thr Leu Asp Leu Phe Phe Ala Gly Thr Glu Thr Thr Ser Thr Thr	
275 280 285	
ctg cga tgg gct ctg ctt tat atg gcc ctc tac cca gaa atc caa gaa	912
Leu Arg Trp Ala Leu Leu Tyr Met Ala Leu Tyr Pro Glu Ile Gln Glu	
290 295 300	

aaa gta caa gtc gag att gac aga gtg att ggc cag ggg cag cag ccg 960
 Lys Val Gln Val Glu Ile Asp Arg Val Ile Gly Gln Gly Gln Gln Pro
 305 310 315 320

agc aca gcc gcc cgg gag tcc atg ccc tac acc aat gct gtc atc cat 1008
 Ser Thr Ala Ala Arg Glu Ser Met Pro Tyr Thr Asn Ala Val Ile His
 325 330 335

gag gtg cag agt 1020
 Glu Val Gln Ser
 340

<210> 2
 <211> 340
 <212> PRT
 <213> Homo sapiens

<400> 2

Ala Asp Phe Leu Lys Arg Arg Arg Pro Lys Asn Tyr Pro Pro Gly Pro
 1 5 10 15

Trp Arg Leu Pro Phe Leu Gly Asn Phe Phe Leu Val Asp Phe Glu Gln
 20 25 30

Ser His Leu Glu Val Gln Leu Phe Val Lys Lys Tyr Gly Asn Leu Phe
 35 40 45

Ser Leu Glu Leu Gly Asp Ile Ser Ala Val Leu Ile Thr Gly Leu Pro
 50 55 60

Leu Ile Lys Glu Ala Leu Ile His Met Asp Gln Asn Phe Gly Asn Arg
 65 70 75 80

Pro Val Thr Pro Met Arg Glu His Ile Phe Lys Lys Asn Gly Leu Ile
 85 90 95

Met Ser Ser Gly Gln Ala Trp Lys Glu Gln Arg Arg Phe Thr Leu Thr
 100 105 110

Ala Leu Arg Asn Phe Gly Leu Gly Lys Lys Gly Leu Glu Glu Arg Ile
 115 120 125

Gln Glu Glu Ala Gln His Leu Thr Glu Ala Ile Lys Glu Glu Asn Gly
 130 135 140

Gln Pro Phe Asp Pro His Phe Lys Ile Asn Asn Ala Val Ser Asn Ile
 145 150 155 160

Ile Cys Ser Ile Thr Phe Gly Glu Arg Phe Glu Tyr Gln Asp Ser Trp
 165 170 175

Phe Gln Gln Leu Leu Lys Leu Leu Asp Glu Val Thr Tyr Leu Glu Ala
 180 185 190

Ser Lys Thr Cys Gln Leu Tyr Asn Val Phe Pro Trp Ile Met Lys Phe
 195 200 205

Leu Pro Gly Pro His Gln Thr Leu Phe Ser Asn Trp Lys Lys Leu Lys
 210 215 220

Leu Phe Val Ser His Met Ile Asp Lys His Arg Lys Asp Trp Asn Pro
 225 230 235 240

Ala Glu Thr Arg Asp Phe Ile Asp Ala Tyr Leu Lys Glu Met Ser Lys
 245 250 255

His Thr Gly Asn Pro Thr Ser Ser Phe His Glu Glu Asn Leu Ile Cys
 260 265 270

Ser Thr Leu Asp Leu Phe Phe Ala Gly Thr Glu Thr Thr Ser Thr Thr
 275 280 285

Leu Arg Trp Ala Leu Leu Tyr Met Ala Leu Tyr Pro Glu Ile Gln Glu
 290 295 300

Lys Val Gln Val Glu Ile Asp Arg Val Ile Gly Gln Gly Gln Gln Pro
 305 310 315 320

Ser Thr Ala Ala Arg Glu Ser Met Pro Tyr Thr Asn Ala Val Ile His
 325 330 335

Glu Val Gln Ser
 340

<210> 3
 <211> 20
 <212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 3

gctgactttc tcaaaagacg

20

<210> 4

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 4

ctctgcacct catggatgac

20